RNAbrowse

user manual

Version table

Version	Authors	Date	Modifications	Remarks
0.1	CK	June 14th, 2013	Initial version	
0.2	CN & CK	July 17th, 2013	Screen-shots, definitions	
0.3	CK	October 23rd, 2013	New screen-shots	

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Introduction

The RNAbrowse is a user oriented web environment presenting analysis results performed after a de novo assembly of transcriptomic reads. It is centred on two data types : contigs and variations (SNP & Indels). For each data types, it displays different views presenting analysis results, in a easily understandable form, for final users wishing to extract biological meaningful knowledge.

The environment is build upon the biomart framework. BioMart (http://www.biomart.org/) is a freely available, open source, federated database system that provides unified access to disparate, geographically distributed data sources. It is designed to be data agnostic and platform independent, such that existing databases can easily be incorporated into the BioMart framework.

RNAbrowse is organised to present the datasets first in a global graphical manner (general statistics) before exploring each individual contig or variation. In the same way the contig or variation visualisation parts are entered through a summary linking to several more detailed views.

The system has been build to be easily extendible. First new graphics can be added to the statistical views, second new databases annotation results can be uploaded and queried, last third new analysis pages can be developed and added to any section. The first pages (general and dataset) can be customized to give informations about the corresponding project.

This document presents all the functions of the environment giving examples when needed of how to use it.

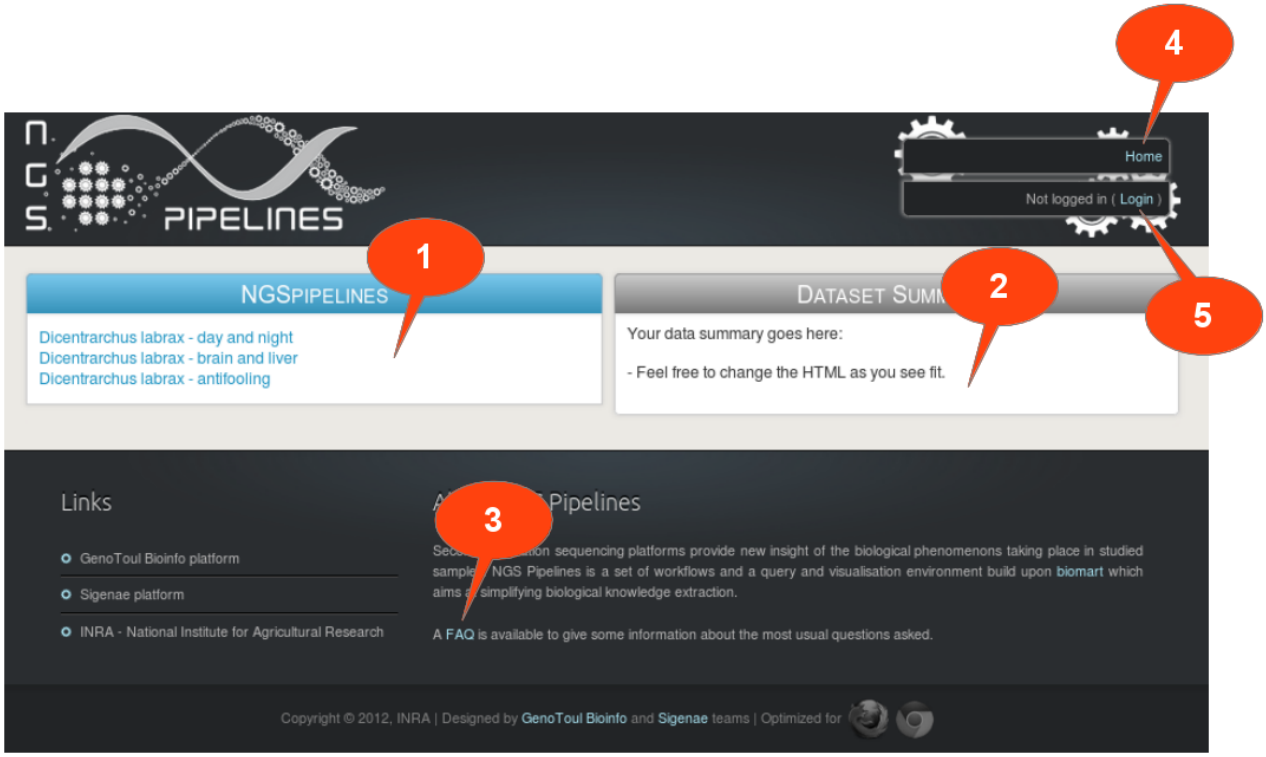
RNAbrowse is in its first version and many improvements can be made. So please feel free to ask questions (support.genopole@toulouse.inra.fr) and modifications or new features using our forge tracker :https://mulcyber.toulouse.inra.fr/pm/task.php?group_project_id=527&group_id=149&func=browse .

General layout

The general layout section give an overview of the two first pages encountered when entering the environment. These page correspond to the home page of the website and the dataset pages which give individual access to each dataset loaded in RNAbrowse.

Home page

The first screen-shot hereunder presents the home page of the environment. To see what it looks like in you web-browser you can open : http://ngspipelines.toulouse.inra.fr:9000/


4
PIPELINES
Home
Not logged in (Login)
1
2
5
NGSPIPELINES
Dicentrarchus labrax - day and night
Dicentrarchus labrax - brain and liver
Dicentrarchus labrax - antifooling
DATASET SUMM
Your data summary goes here:
- Feel free to change the HTML as you see fit.
Links
GenoToul Bioinfo platform
Sigenae platform
INRA - National Institute for Agricultural Research
3
Pipelines
sequencing platforms provide new insight of the biological phenomenons taking place in studied
NGS Pipelines is a set of workflows and a query and visualisation environment build upon biomart which
simplifying biological knowledge extraction.
A FAQ is available to give some information about the most usual questions asked.
Copyright © 2012, INRA | Designed by GenoToul Bioinfo and Sigenae teams | Optimized for

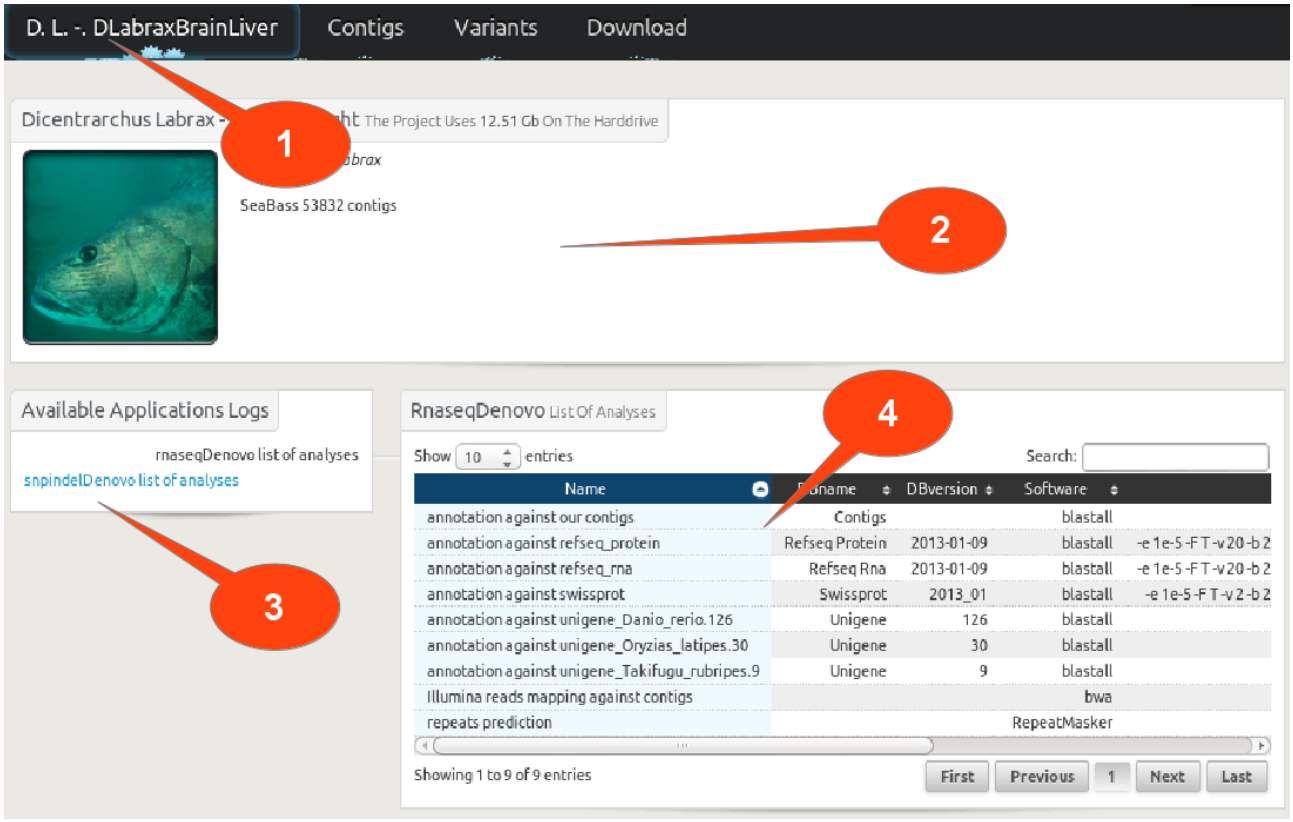
The elements numbered in the above presented screen-shot correspond to :

1. different datasets loaded in RNAbrowse,
2. customizable page element in which global information on the project or the laboratory having produced the data can be displayed,
3. link the the FAQ (frequently asked questions),
4. link to the home page and page tree location,
5. OpenID login access (biomart function **not implemented yet**).

NB. The page header and footer (dark gray) are displayed on all pages.

Dataset page

The dataset page gives different informations on the dataset which has been assembled and annotated.



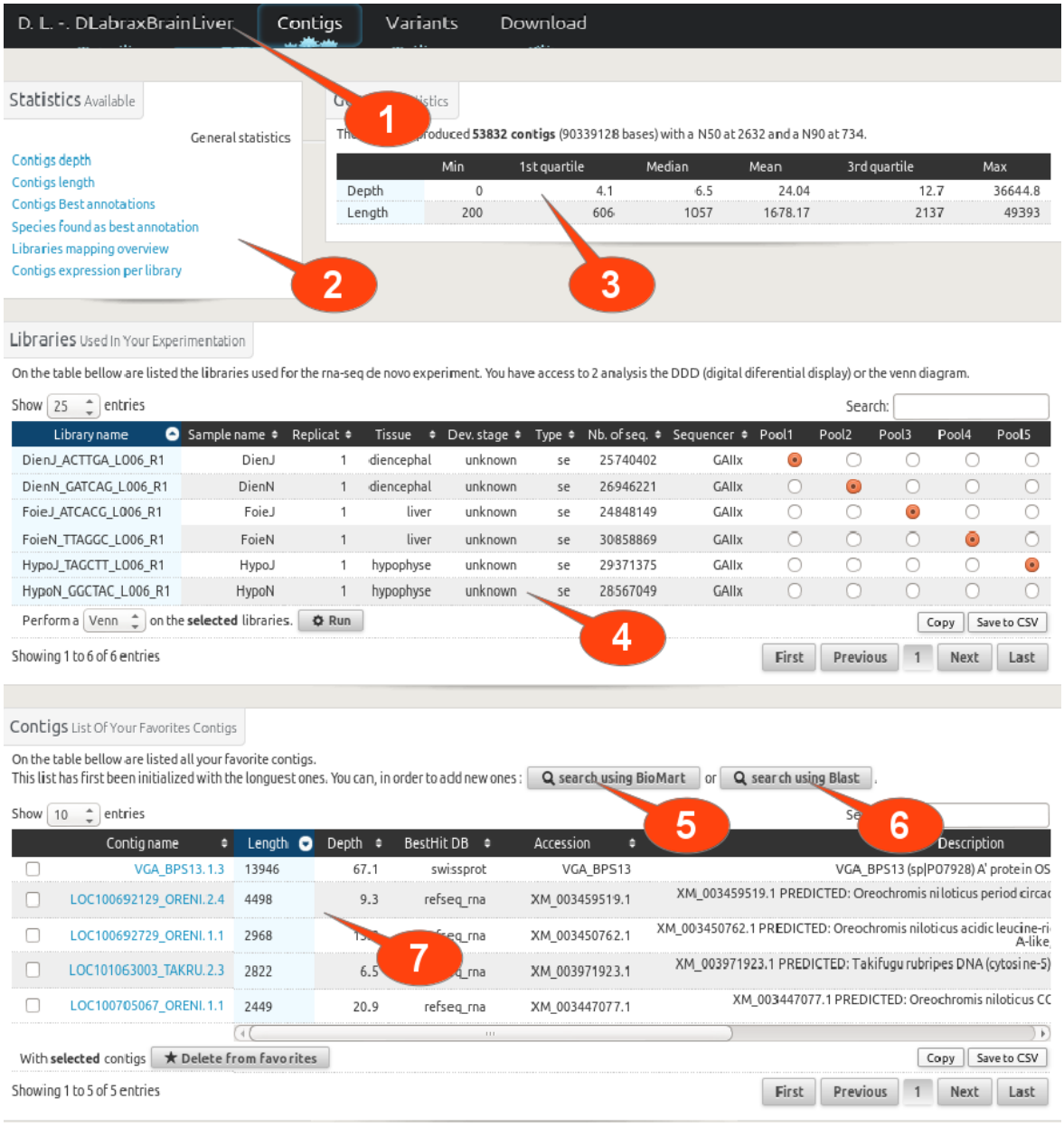
The elements numbered in the screen-shot above correspond to :

1. the general menu of the dataset,
2. the presentation block which can be customized according to the needs,
3. the application log menu,
4. the application log itself. It includes all the processing steps the data has undergone, including the database name and version when relevant, the software packages used and the parameters as well as the dates of processing.

The bottom sections of the page aims at simplifying the “material and method” writing for the future articles using this dataset.

Assembly part (Contigs)

From the dataset page, the user can access the assembly and annotation results using the Contigs menu item.


D. L. -. DLabraxBrainLiver
Contigs
Variants
Download
Statistics Available
General statistics
Contigs depth
Contigs length
Contigs Best annotations
Species found as best annotation
Libraries mapping overview
Contigs expression per library
produced 53832 contigs (90339128 bases) with a N50 at 2632 and a N90 at 734.
Min 1st quartile Median Mean 3rd quartile Max
Depth 0 4.1 6.5 24.04 12.7 36644.8
Length 200 606 1057 1678.17 2137 49393
1
2
3
Libraries Used In Your Experimentation
On the table bellow are listed the libraries used for the rna-seq de novo experiment. You have access to 2 analysis the DDD (digital diferential display) or the venn diagram.
Show 25 entries
Search:
Library name Sample name Replicat Tissue Dev. stage Type Nb. of seq. Sequencer Pool1 Pool2 Pool3 Pool4 Pool5
DienJ_ACTTGA_L006_R1 DienJ 1 diencephal unknown se 25740402 GAIIx
DienN_GATCAG_L006_R1 DienN 1 diencephal unknown se 26946221 GAIIx
FoieJ_ATCACG_L006_R1 FoieJ 1 liver unknown se 24848149 GAIIx
FoieN_TTAGGC_L006_R1 FoieN 1 liver unknown se 30858869 GAIIx
HypoJ_TAGCTT_L006_R1 HypoJ 1 hypophyse unknown se 29371375 GAIIx
HypoN_GGCTAC_L006_R1 HypoN 1 hypophyse unknown se 28567049 GAIIx
Perform a Venn on the selected libraries. Run
Copy Save to CSV
Showing 1 to 6 of 6 entries
First Previous 1 Next Last
4
Contigs List Of Your Favorites Contigs
On the table bellow are listed all your favorite contigs.
This list has first been initialized with the longuest ones. You can, in order to add new ones : search using BioMart or search using Blast .
Show 10 entries
Contig name Length Depth BestHit DB Accession Description
VGA_BPS13.1.3 13946 67.1 swissprot VGA_BPS13 VGA_BPS13 (sp|P07928) A' protein OS
LOC100692129_ORENI.2.4 4498 9.3 refseq_rna XM_003459519.1 XM_003459519.1 PREDICTED: Oreochromis niloticus period circac
LOC100692729_ORENI.1.1 2968 refseq_rna XM_003450762.1 XM_003450762.1 PREDICTED: Oreochromis niloticus acidic leucine-ri A-like
LOC101063003_TAKRU.2.3 2822 6.5 rna XM_003971923.1 XM_003971923.1 PREDICTED: Takifugu rubripes DNA (cytosine-5)
LOC100705067_ORENI.1.1 2449 20.9 refseq_rna XM_003447077.1 XM_003447077.1 PREDICTED: Oreochromis niloticus CC
5
6
7
With selected contigs Delete from favorites
Copy Save to CSV
Showing 1 to 5 of 5 entries
First Previous 1 Next Last

The elements numbered in the here-over presented screen-shot correspond to :

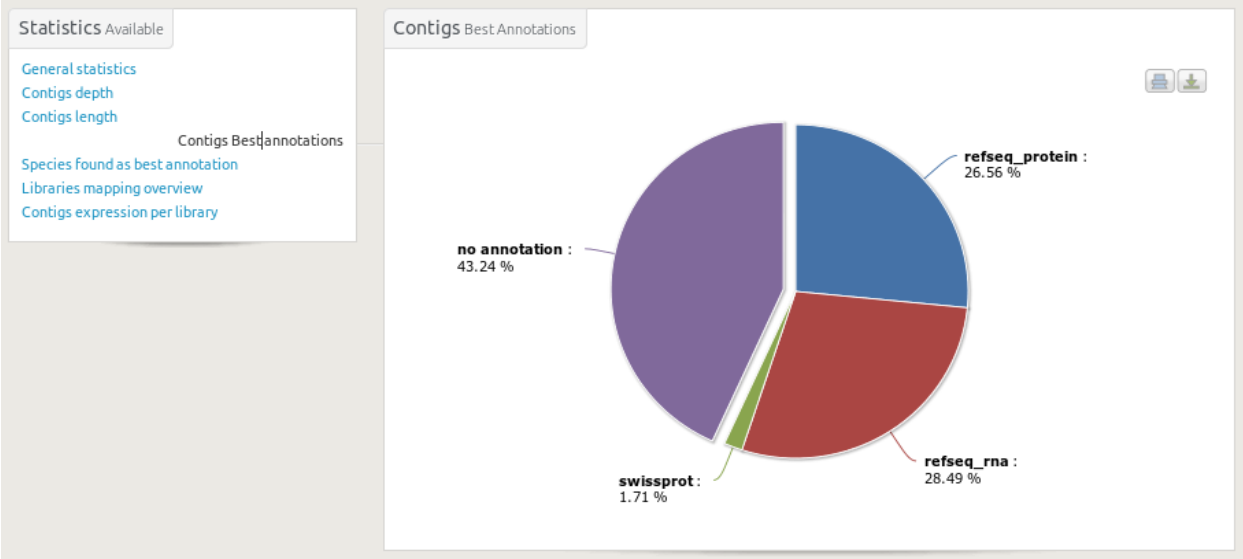
1. menu item to access the contig main page,
2. menu to access various global tables and graphics on the assembly and the annotations,
3. table and graphic display area,
4. library table enabling two analysis :
    1. Venn diagram,

2. DDD (Digital Differential Display),
5. biomart (on attributes or annotation) search button,
6. contigs sequence blast search button,
7. favourite contig table.

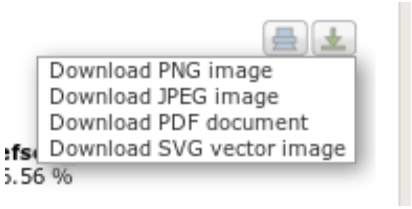
Several of the previously listed elements are presented in the next sections.

Table and graphic display

The top section of the page presents tables or graphics synthesizing information on the contigs. The menu on the left side permits to select the element displayed on the right panel.



The graphics can be printed or downloaded in four different formats.

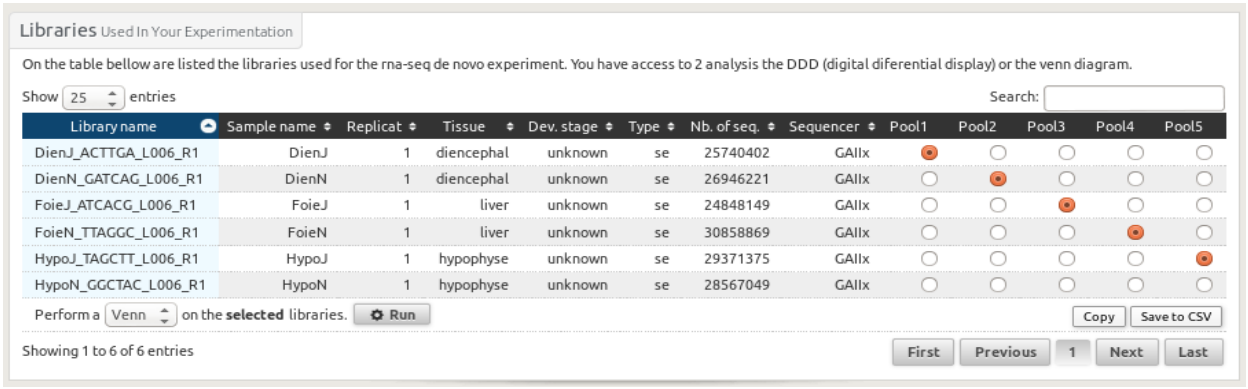


Library table

The library table displays all the samples used in the assembly or alignment processing phases. It includes informations about the replicate number, the tissue, the development stage, the sequencer, the read type (singled-ends or paired-ends), the number of reads.

If the library table has more than 20 lines, they will be presented on several pages. Four button at the bottom right side of the table enable to move from one page to the next, the previous, the first or the last page. You can also move in the table by clicking on the page number buttons.

The table can be copied to the clipboard and saved as a csv file using the buttons above the navigation buttons presented in the previous paragraph.


Libraries Used In Your Experimentation
On the table bellow are listed the libraries used for the rna-seq de novo experiment. You have access to 2 analysis the DDD (digital diferential display) or the venn diagram.
Show 25 entries
Search:
Library name | Sample name | Replicat | Tissue | Dev. stage | Type | Nb. of seq. | Sequencer | Pool1 | Pool2 | Pool3 | Pool4 | Pool5
DienJ_ACTTGA_L006_R1 | DienJ | 1 | diencephal | unknown | se | 25740402 | GAIIx
DienN_GATCAG_L006_R1 | DienN | 1 | diencephal | unknown | se | 26946221 | GAIIx
FoieJ_ATCACG_L006_R1 | FoieJ | 1 | liver | unknown | se | 24848149 | GAIIx
FoieN_TTAGGC_L006_R1 | FoieN | 1 | liver | unknown | se | 30858869 | GAIIx
HypoJ_TAGCTT_L006_R1 | HypoJ | 1 | hypophyse | unknown | se | 29371375 | GAIIx
HypoN_GGCTAC_L006_R1 | HypoN | 1 | hypophyse | unknown | se | 28567049 | GAIIx
Perform a Venn on the selected libraries. Run
Copy
Save to CSV
Showing 1 to 6 of 6 entries
First
Previous
1
Next
Last

The table can also be used to launch two types of analysis :

- Venn diagram
- Digital Differential Display (DDD).

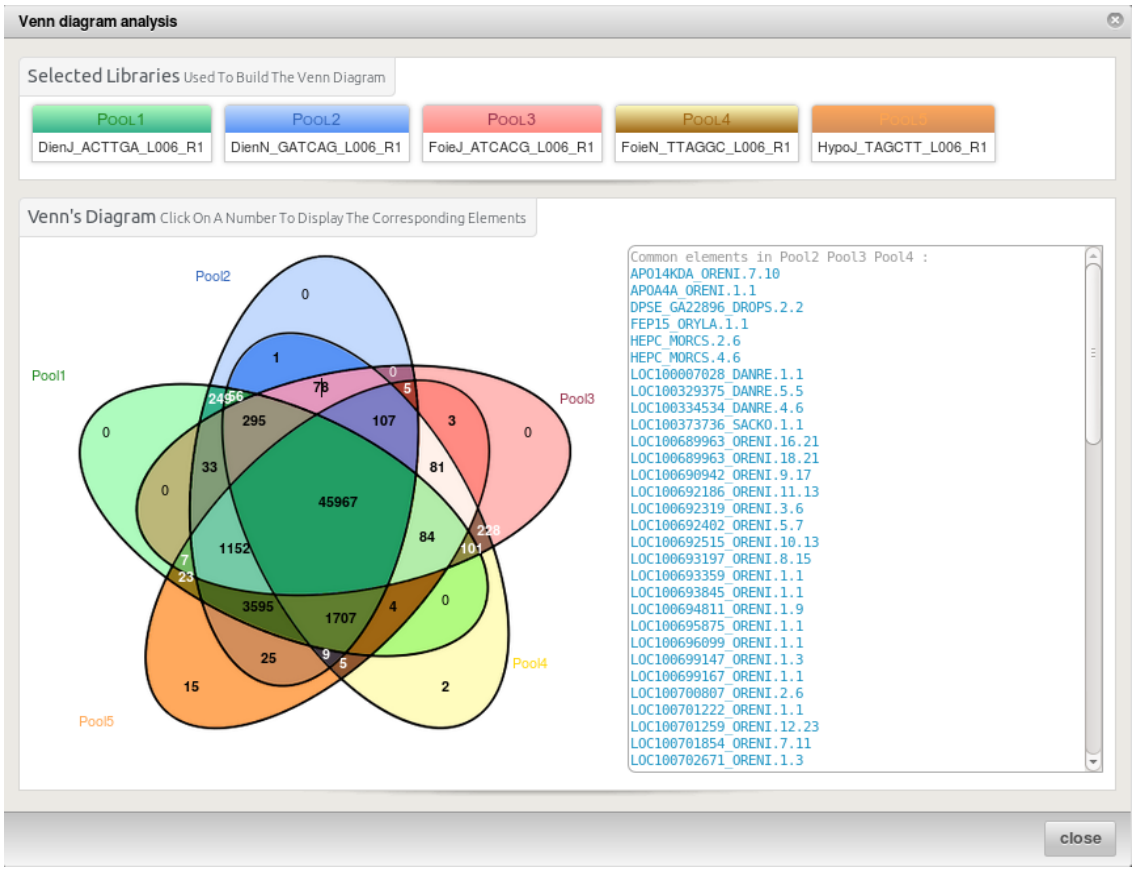
Venn diagram analysis

The Venn diagram shows the number of contigs shared between libraries and the ones which are specific to a library for which only sequences of this library are aligned on the contig. To build a new diagram the user has to select the libraries he wants to have in each pool (from two to five), then select Venn in the bottom left menu and click the run button. A new frame will appear. In this frame, a spinning wheel will inform you that the job is been processed. Once the result is available, it will be displayed as shown in the next screen-shot.

The libraries used in each pool are listed in the table on the top of the frame with the corresponding colour in the diagram.

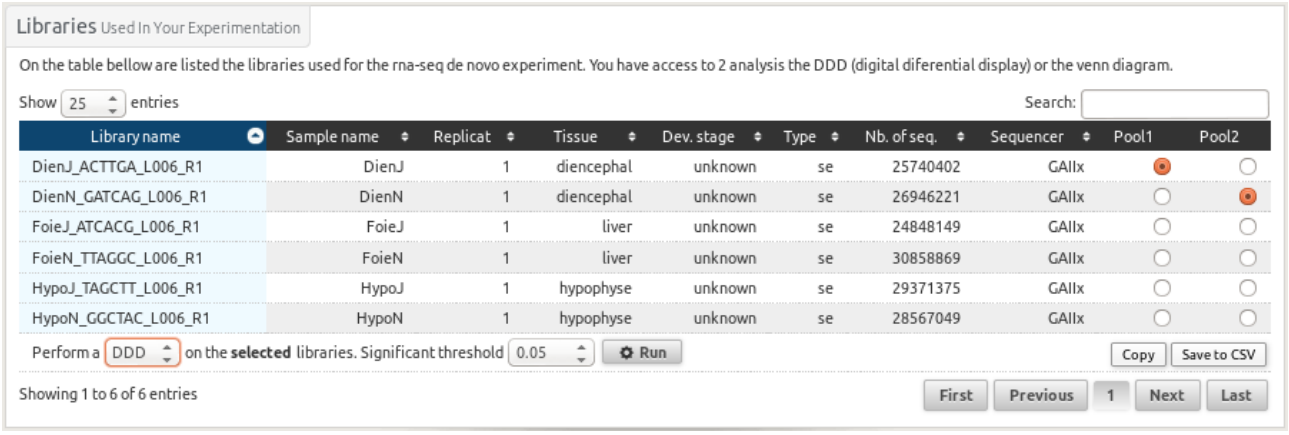
If you click on a figure in the graph the list of corresponding contigs will appear in the list box on the right hand side of the frame. The contig names are links to the corresponding pages.

To close the frame (light box) use the cross located in the top right corner or the 'close' button at the right side of the frame. This is true for all frames.



Digital differential display (DDD)

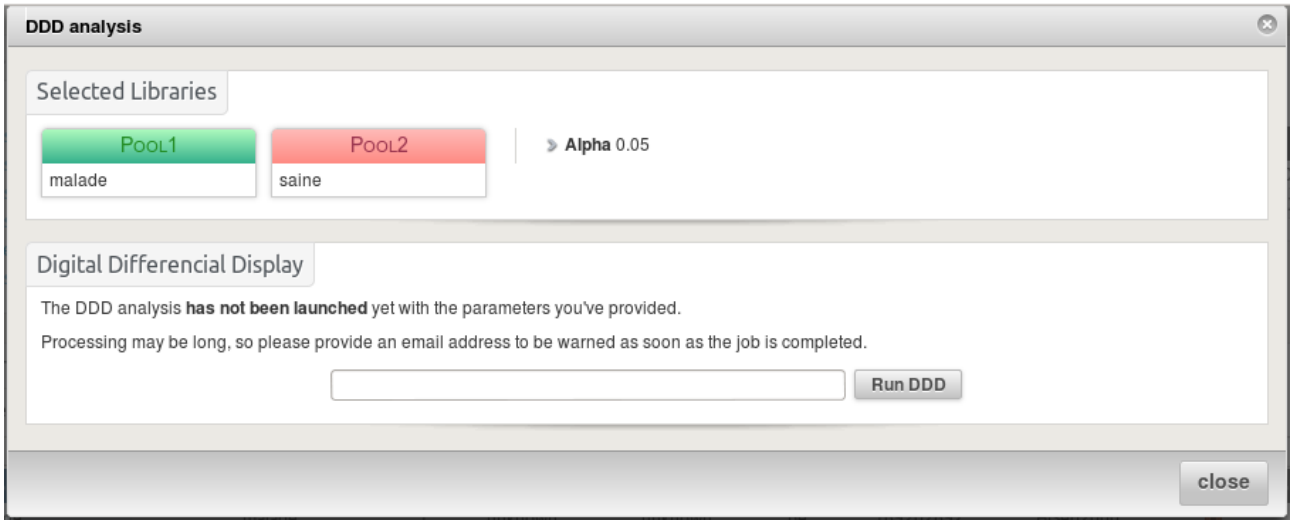
From the library table it is also possible to launch a digital differential display analysis. First select DDD in the bottom left menu. This will limit the layout of the left columns of the table to two pools.


Libraries Used In Your Experimentation
On the table bellow are listed the libraries used for the rna-seq de novo experiment. You have access to 2 analysis the DDD (digital diferential display) or the venn diagram.
Show 25 entries
Search:
Library name
Sample name
Replicat
Tissue
Dev. stage
Type
Nb. of seq.
Sequencer
Pool1
Pool2
DienJ_ACTTGA_L006_R1 DienJ 1 diencephal unknown se 25740402 GAIIx
DienN_GATCAG_L006_R1 DienN 1 diencephal unknown se 26946221 GAIIx
FoieJ_ATCACG_L006_R1 FoieJ 1 liver unknown se 24848149 GAIIx
FoieN_TTAGGC_L006_R1 FoieN 1 liver unknown se 30858869 GAIIx
HypoJ_TAGCTT_L006_R1 HypoJ 1 hypophyse unknown se 29371375 GAIIx
HypoN_GGCTAC_L006_R1 HypoN 1 hypophyse unknown se 28567049 GAIIx
Perform a DDD on the selected libraries. Significant threshold 0.05
Run
Copy
Save to CSV
Showing 1 to 6 of 6 entries
First
Previous
1
Next
Last

Then select the libraries to be merged in the pools. Select the significance threshold you want

to use (five values are available : 0.05, 0.02, 0.01, 0.001 and 0.0001). Then click on the run button. The following frame will appear.

This frame shows the selected library pools with the corresponding colours and invite you to enter your e-mail address because of the time needed to process the data.


DDD analysis
Selected Libraries
Pool1
malade
Pool2
saine
Alpha 0.05
Digital Differencial Display
The DDD analysis has not been launched yet with the parameters you've provided.
Processing may be long, so please provide an email address to be warned as soon as the job is completed.
Run DDD
close

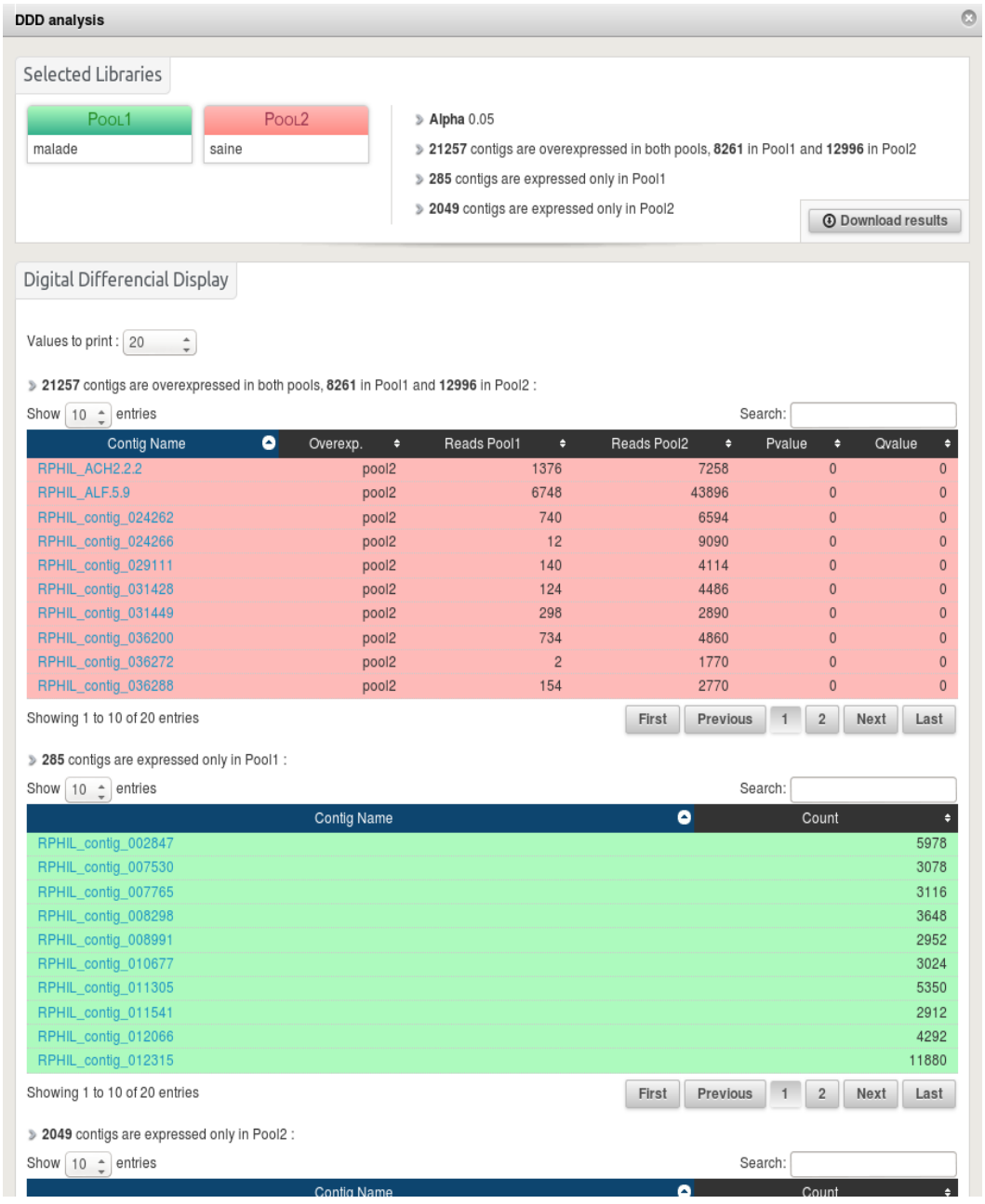
Once the processing is finished an e-mail will be sent to your address. This e-mail contains a link to the DDD results.

```
Hello,

The ddd analysis you have launched is complete
To see your results click on this link : http://ngspipelines-sigenae.toulouse.inra.fr:9000/ngspipelines/#!/NGSpipelines/Ruditapes%20philippinarum?actDataset=rnaseqDenovo&dddAnalysisIDKey=18

Please do no respond to this mail
```

Clicking on the link will redirect you to the corresponding web page (example shown on the next page). The result page contains four parts :

1. The top page block presents the informations about the chosen library pools, the selected significance threshold and the general figures about the number of contigs over-expressed contigs in either pools or expressed in only one of the pools. It also includes the links to download the complete results set containing eight files out of which three can be used to query GO terms at the Wego website : http://wego.genomics.org.cn .
    1. expressed_only_in_pool2.wego
    2. expressed_only_in_pool1.wego
    3. expressed_only_in_pool2.tsv
    4. overexpressed_only_in_pool1.wego
    5. overexpressed_only_in_pool2.wego
    6. expressed_only_in_pool1.tsv
    7. overexpressed_only_in_pool1.tsv
    8. overexpressed_only_in_pool2.tsv

2. The second block presents 20 contigs over-expressed in pool 1.
3. The third block presents 20 contigs over-expressed in pool 2.
4. The fourth block presents 20 contigs only expressed in pool 1.
5. The fifth block presents 20 contigs only expressed in pool 2.

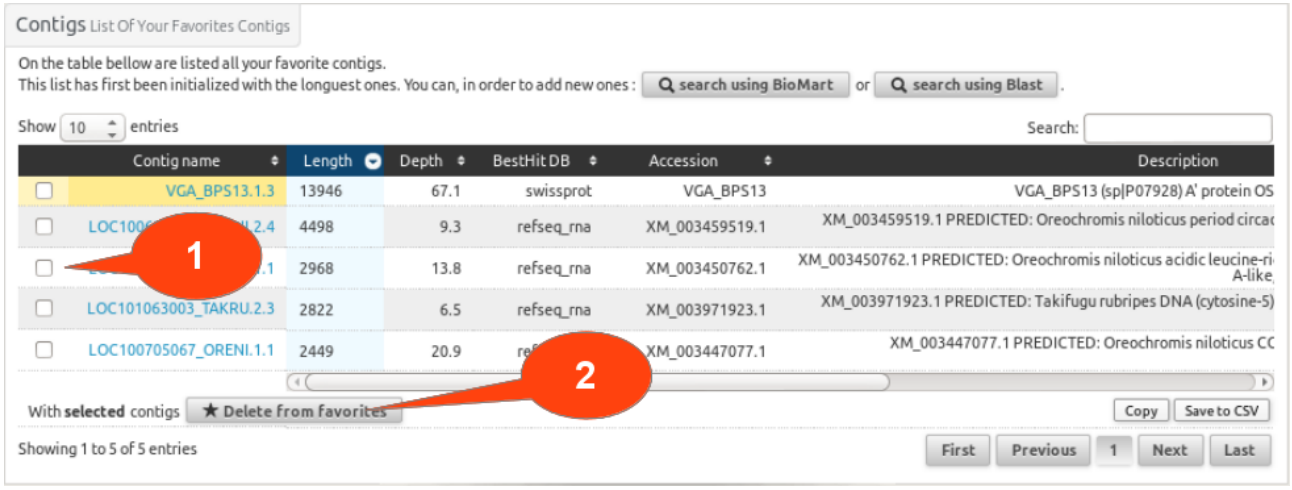

DDD analysis
Selected Libraries
Pool1
malade
Pool2
saine
Alpha 0.05
21257 contigs are overexpressed in both pools, 8261 in Pool1 and 12996 in Pool2
285 contigs are expressed only in Pool1
2049 contigs are expressed only in Pool2
Download results
Digital Differencial Display
Values to print : 20
21257 contigs are overexpressed in both pools, 8261 in Pool1 and 12996 in Pool2 :
Show 10 entries
Search:
Contig Name | Overexp. | Reads Pool1 | Reads Pool2 | Pvalue | Qvalue
RPHIL_ACH2.2.2 pool2 1376 7258 0 0
RPHIL_ALF.5.9 pool2 6748 43896 0 0
RPHIL_contig_024262 pool2 740 6594 0 0
RPHIL_contig_024266 pool2 12 9090 0 0
RPHIL_contig_029111 pool2 140 4114 0 0
RPHIL_contig_031428 pool2 124 4486 0 0
RPHIL_contig_031449 pool2 298 2890 0 0
RPHIL_contig_036200 pool2 734 4860 0 0
RPHIL_contig_036272 pool2 2 1770 0 0
RPHIL_contig_036288 pool2 154 2770 0 0
Showing 1 to 10 of 20 entries
First Previous 1 2 Next Last
285 contigs are expressed only in Pool1 :
Show 10 entries
Search:
Contig Name | Count
RPHIL_contig_002847 5978
RPHIL_contig_007530 3078
RPHIL_contig_007765 3116
RPHIL_contig_008298 3648
RPHIL_contig_008991 2952
RPHIL_contig_010677 3024
RPHIL_contig_011305 5350
RPHIL_contig_011541 2912
RPHIL_contig_012066 4292
RPHIL_contig_012315 11880
Showing 1 to 10 of 20 entries
First Previous 1 2 Next Last
2049 contigs are expressed only in Pool2 :
Show 10 entries
Search:
Contig Name | Count

Wego Gene Ontology analysis

To perform a wego differential analysis, first uncompress the all_data.zip file, then go the wego website (http://wego.genomics.org.cn) and load the files using the wego native format.

Favorite contig table

This table contains contigs of interest selected by the users. Above the table



Contig can be removed from the favourite table by ticking the checkbox in the first column and pressing the “delete from favourites” button.

The table can be copied to clipboard of downloaded as a CSV file.

Biomart query

Biomart (http://www.biomart.org) is a query environment which permits to make multiple criteria queries. The search page can be access using the “search using biomart” button located at the top of the favourite contig table.

The layout of the search page is presented in the next screen-shot. The search page permits to query all the databases (assemblies) and datasets (contigs or SNP Indels) of the website.

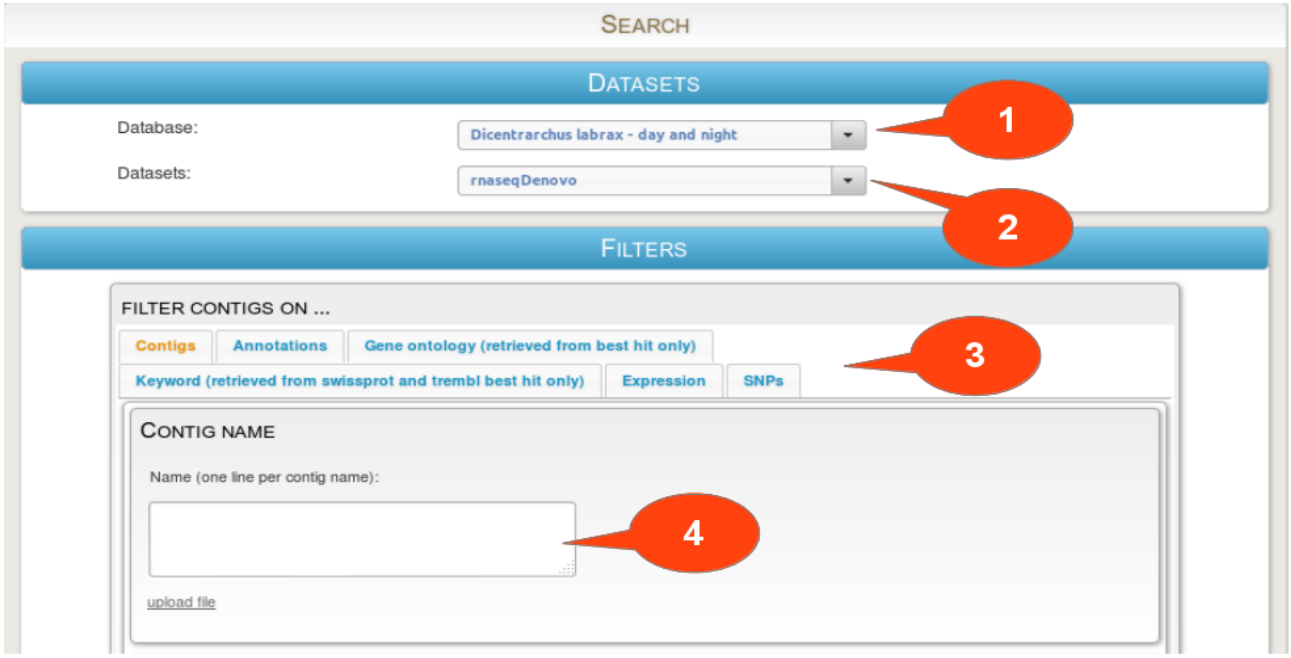
It includes :

1. a database selection menu,
2. a dataset selection menu,
3. a filter block which is organised by data types. To move from one data type to another use the selectors at the page top. The filters are joined with and 'and',
4. An attribute block enabling to select the attributes presented in the result table,
5. the GO button a the bottom of the page to launch the search.

The following screen-shot presents the top elements of the search page :

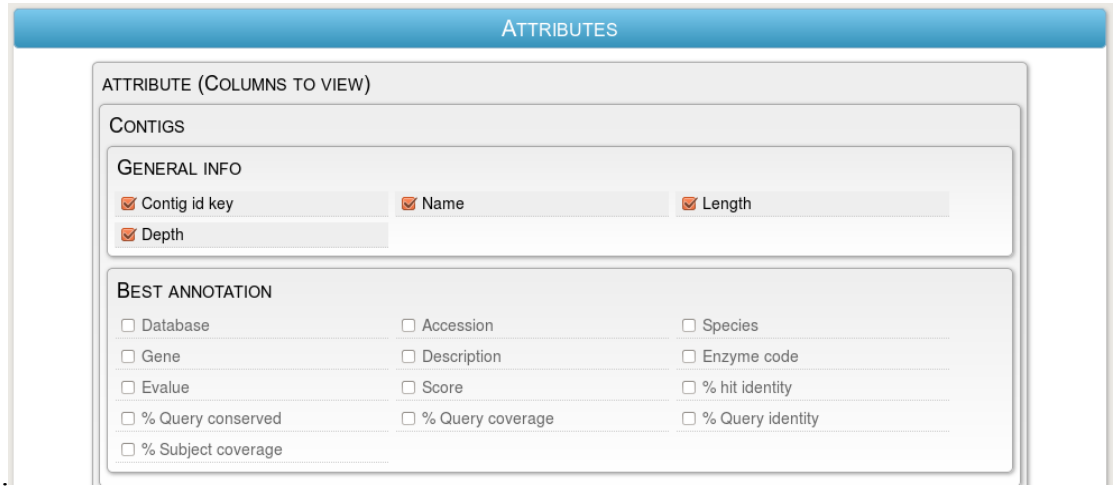
1. a database selection menu

2. a dataset selection menu
3. filter tabs
4. filter on the contig name. This filter can be used by pasting a list of contig names in the entry field or by uploading a file using the link under the entry field.

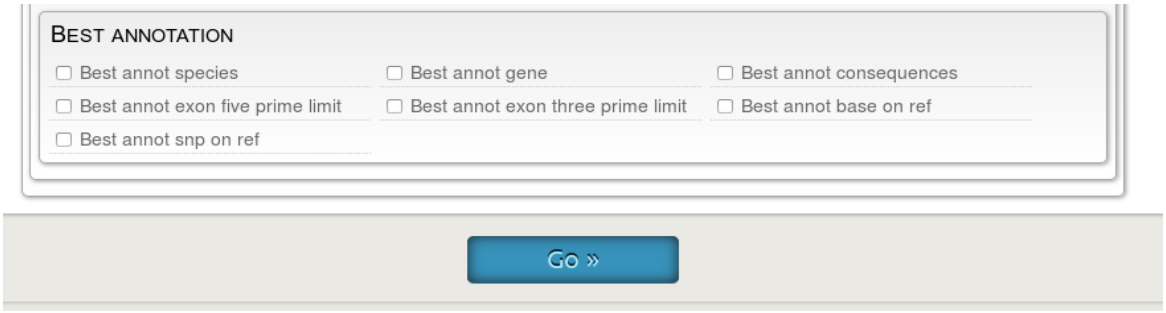


Once a field has been used as a filter (1) a cross appears on the right hand side(2). Click on this cross to remove the filter.

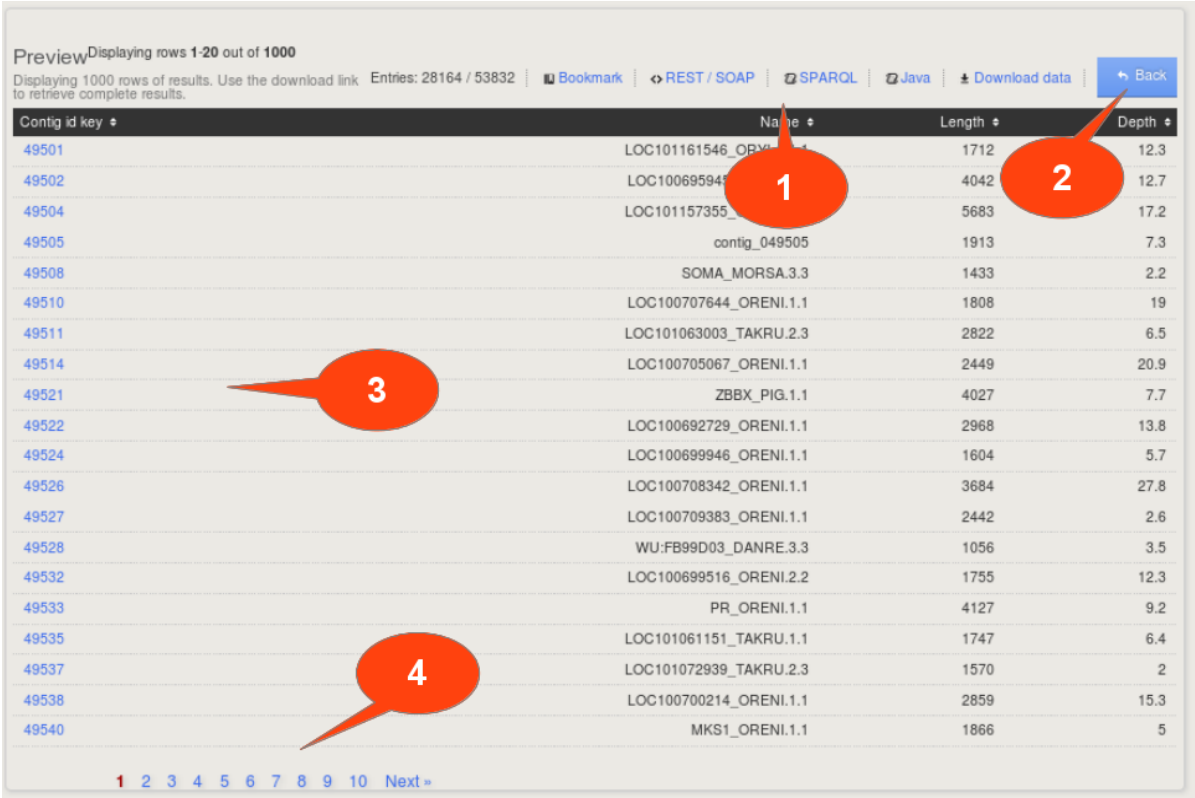
Once the filters have been set, the user has to decide which data will be part of the output table produced by the search. The data are presented in different blocks and chosen by ticking the check boxes located in from of the field names (seen next screen-shot). The fields in the table will be in the order of selection. To change the order you have to untick the boxes are restart the selection process



Once the output data is selected, the user has to click on the “Go” button to launch the search.



The search results are displayed as a table, only the first 1000 lines can be browsed.



The previous screen-shot presents the result table including :

1. different access means to the results of the query :
    1. as a bookmark,
    2. the corresponding REST/SOAP query,
    3. the SPARQL code,
    4. the java code,
    5. the result tabulated text files,
2. the back button to come back to the search page (with the selected options),
3. the result table including links (in blue) when available,
4. the page navigation bar.

BEWARE of the fact that the download file contains a header describing the columns content. This even if you ask for the fasta file of the contigs.

Blast query

The interface also provides a blast search button. The blast is performed on the contig file.

The following screen-shot presents the elements of the blast search page :

1. an entry field to paste the sequence(s), in fasta format, to be blasted (query),
2. the type of blast search (blastn for nucleic sequences, blastx for protein sequences),
3. the expected value filtering the blast results,

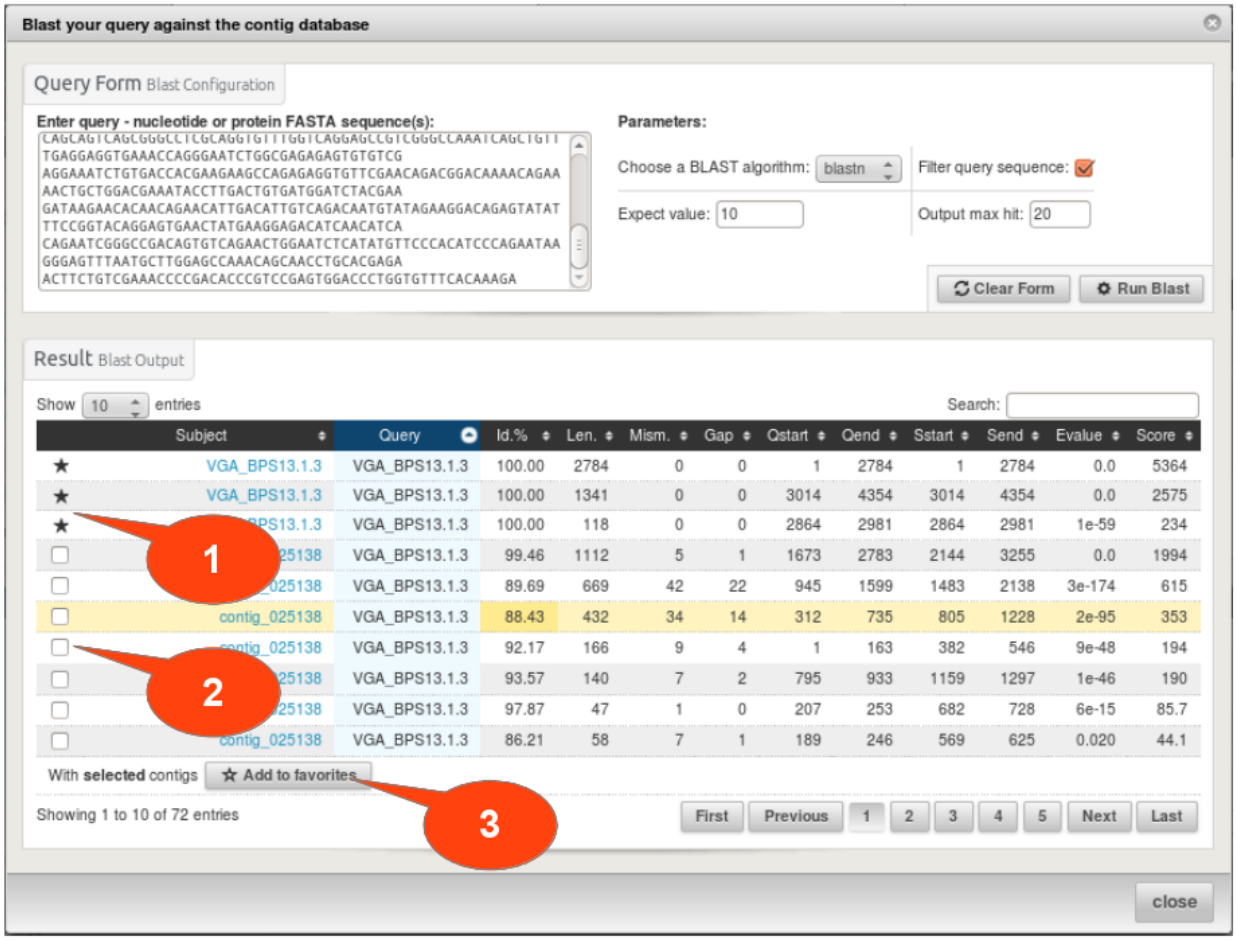
4. the maximum number of outputs to be shown,
5. the clear and run buttons.

The blast results are shown in a table added at the bottom of the search windows presented on the next page.

The blast result table includes the following elements :

1. a column indicating if the contig is part of the favourite (star),
2. this same column enables also to add it to the favourites by ticking the check box,
3. the add to favourite button.

The table can be searched using the box located at the top right part and browsed using the button situated on the bottom right angle.



When you click on a contig from the favourite table or from the biomart query results you open the contig page which will be described in the next chapter.

Contig visualisation

The contig page gives access to different pages including :

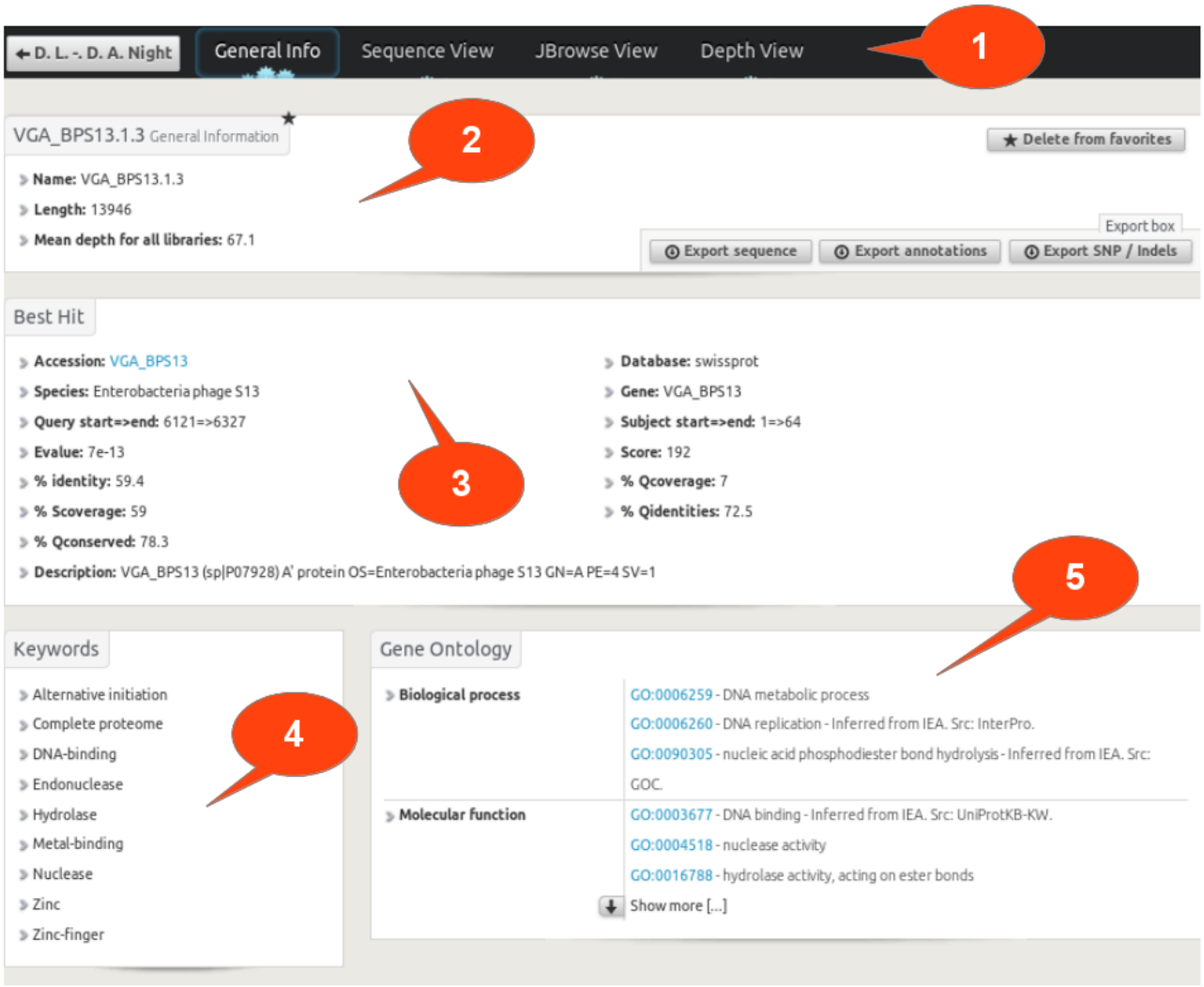
1. general information
2. sequence view
3. jbrowse view
4. depth view

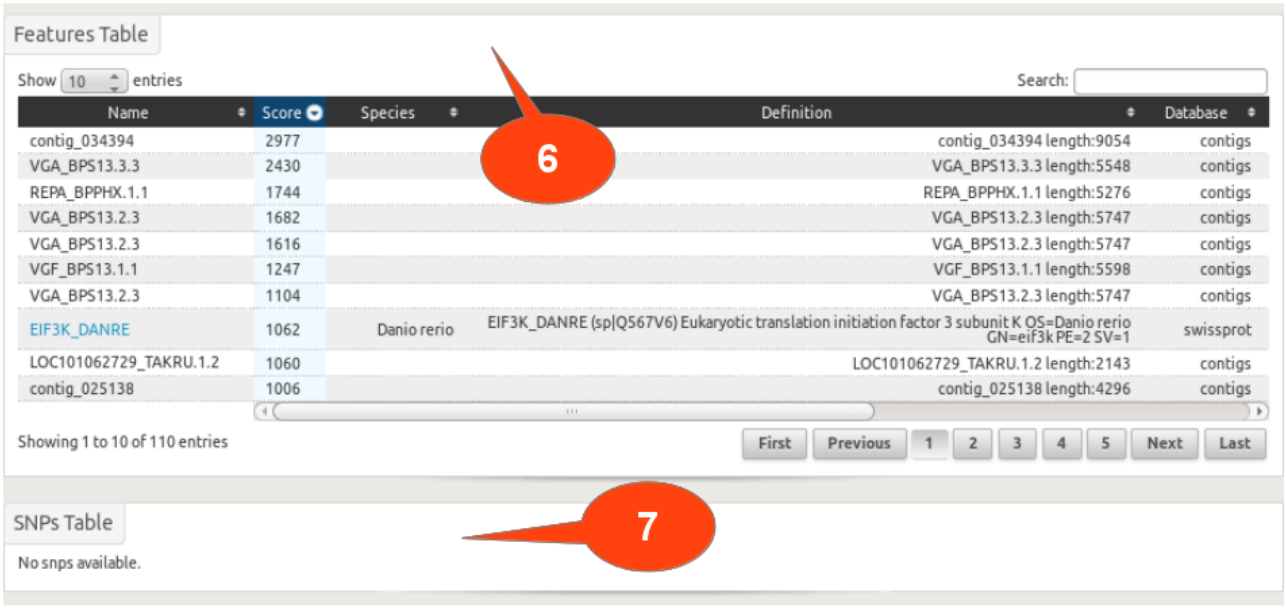
The view are accessed through the menu located on the top of the page and presented in the next screen-shot.

Contig general information page

The first page of the contig section gives general informations about the contigs and its

annotation.


D. L. -. D. A. Night
General Info
Sequence View
JBrowse View
Depth View
1
VGA_BPS13.1.3 General Information
2
Delete from favorites
Name: VGA_BPS13.1.3
Length: 13946
Mean depth for all libraries: 67.1
Export box
Export sequence
Export annotations
Export SNP / Indels
Best Hit
Accession: VGA_BPS13
Species: Enterobacteria phage S13
Query start=>end: 6121=>6327
Evalue: 7e-13
% identity: 59.4
% Scoverage: 59
% Qconserved: 78.3
3
Database: swissprot
Gene: VGA_BPS13
Subject start=>end: 1=>64
Score: 192
% Qcoverage: 7
% Qidentities: 72.5
Description: VGA_BPS13 (sp|P07928) A' protein OS=Enterobacteria phage S13 GN=A PE=4 SV=1
5
Keywords
Alternative initiation
Complete proteome
DNA-binding
Endonuclease
Hydrolase
Metal-binding
Nuclease
Zinc
Zinc-finger
4
Gene Ontology
Biological process
GO:0006259 - DNA metabolic process
GO:0006260 - DNA replication - Inferred from IEA. Src: InterPro.
GO:0090305 - nucleic acid phosphodiester bond hydrolysis - Inferred from IEA. Src: GOC.
Molecular function
GO:0003677 - DNA binding - Inferred from IEA. Src: UniProtKB-KW.
GO:0004518 - nuclease activity
GO:0016788 - hydrolase activity, acting on ester bonds
Show more [...]


Features Table
Show 10 entries
Search:
Name
Score
Species
Definition
Database
contig_034394 2977 contig_034394 length:9054 contigs
VGA_BPS13.3.3 2430 VGA_BPS13.3.3 length:5548 contigs
REPA_BPPHX.1.1 1744 REPA_BPPHX.1.1 length:5276 contigs
VGA_BPS13.2.3 1682 VGA_BPS13.2.3 length:5747 contigs
VGA_BPS13.2.3 1616 VGA_BPS13.2.3 length:5747 contigs
VGF_BPS13.1.1 1247 VGF_BPS13.1.1 length:5598 contigs
VGA_BPS13.2.3 1104 VGA_BPS13.2.3 length:5747 contigs
EIF3K_DANRE 1062 Danio rerio EIF3K_DANRE (sp|Q567V6) Eukaryotic translation initiation factor 3 subunit K OS=Danio rerio GN=eif3k PE=2 SV=1 swissprot
LOC101062729_TAKRU.1.2 1060 LOC101062729_TAKRU.1.2 length:2143 contigs
contig_025138 1006 contig_025138 length:4296 contigs
Showing 1 to 10 of 110 entries
First Previous 1 2 3 4 5 Next Last
6
SNPs Table
No snps available.
7

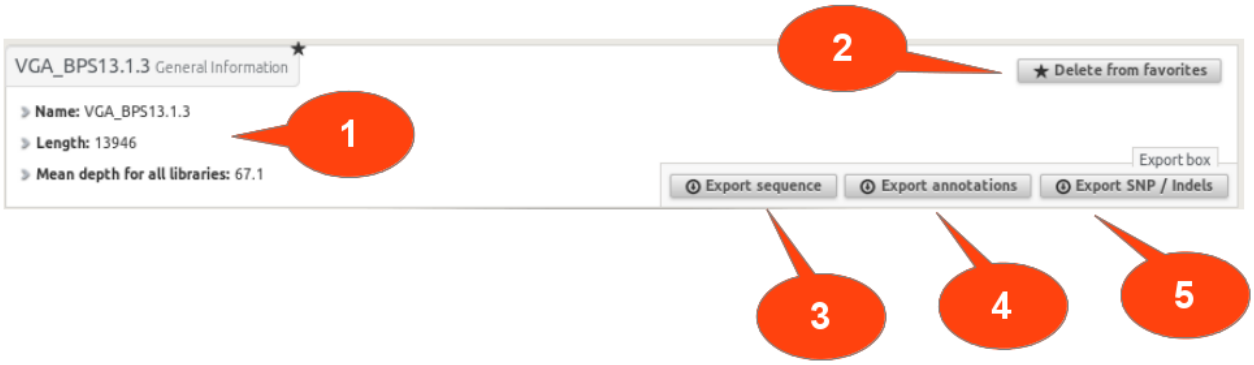
The previous screen-shot presents :

1. the contig menu
2. general information section
3. best hit section
4. Uniprot-Swissprot keyword section
5. GO section
6. annotation section
7. List of SNP/Indels if contig contains it.

At the bottom of this webpage you will also find the SNP Indel section (not shown on the screen-shot).

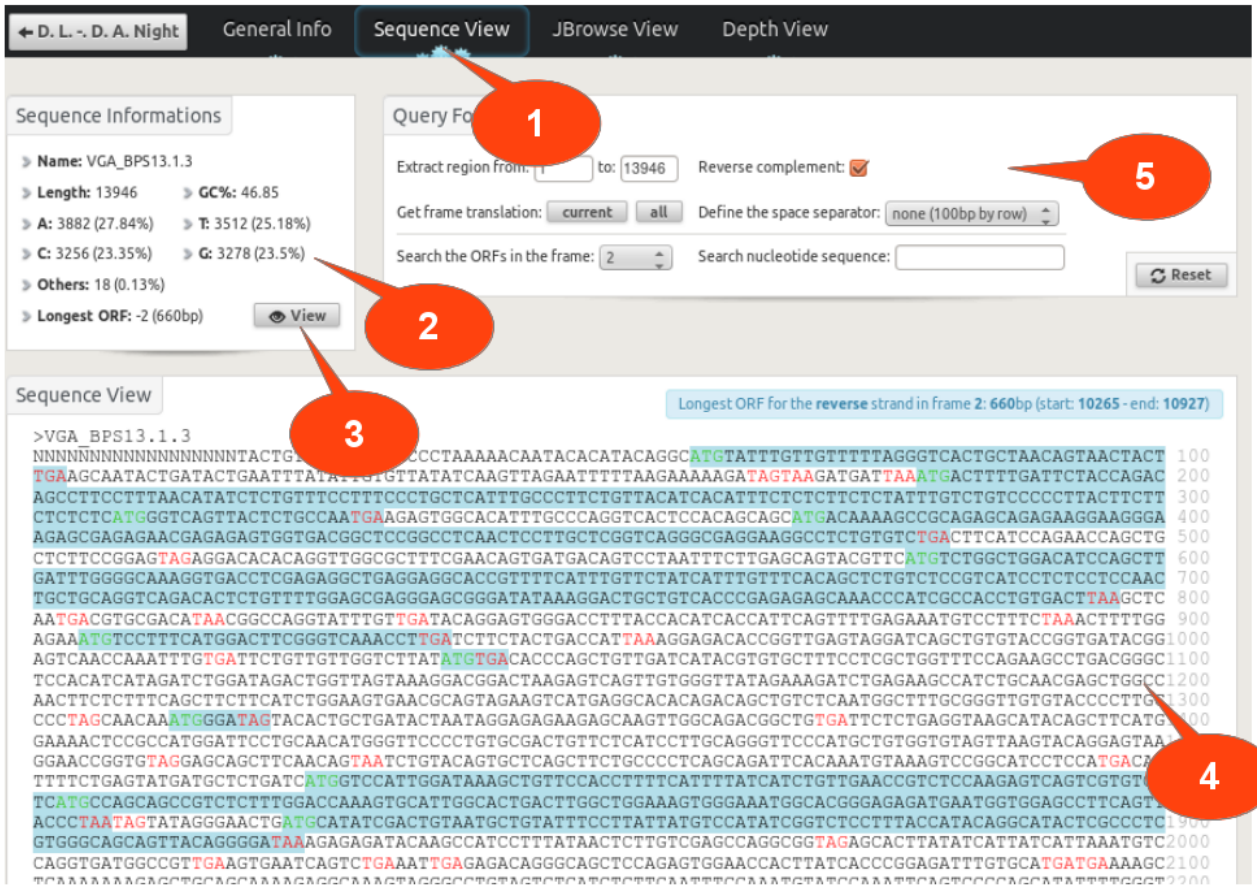
The general information section contains :

1. the name, length and global expression value of the contigs
2. a button to remove this contig from the favourites
3. a button to export the contig sequence in fasta format
4. a button to export the annotation in GFF format
5. a button to export the SNP INDEL of the contig in a tabulate file


VGA_BPS13.1.3 General Information
Name: VGA_BPS13.1.3
Length: 13946
Mean depth for all libraries: 67.1
Delete from favorites
Export box
Export sequence
Export annotations
Export SNP / Indels
1
2
3
4
5

Contig sequence view

The next page of the contig visualisation part gives access to various informations about the contig sequence and some tools to analyse it.



The screen-shot here over presents :

1. the contig browsing menu
2. the sequence informations such as nucleotide content and longest open reading frame (ORF).
3. The view button presenting the longest ORF in the sequence view
4. the sequence view with possible starts in green, stops in red and ORFs in blue,
5. the query form permitting different action on the sequence such as extraction, reverse complementation, translation in different frames, ORF presentation and text search.

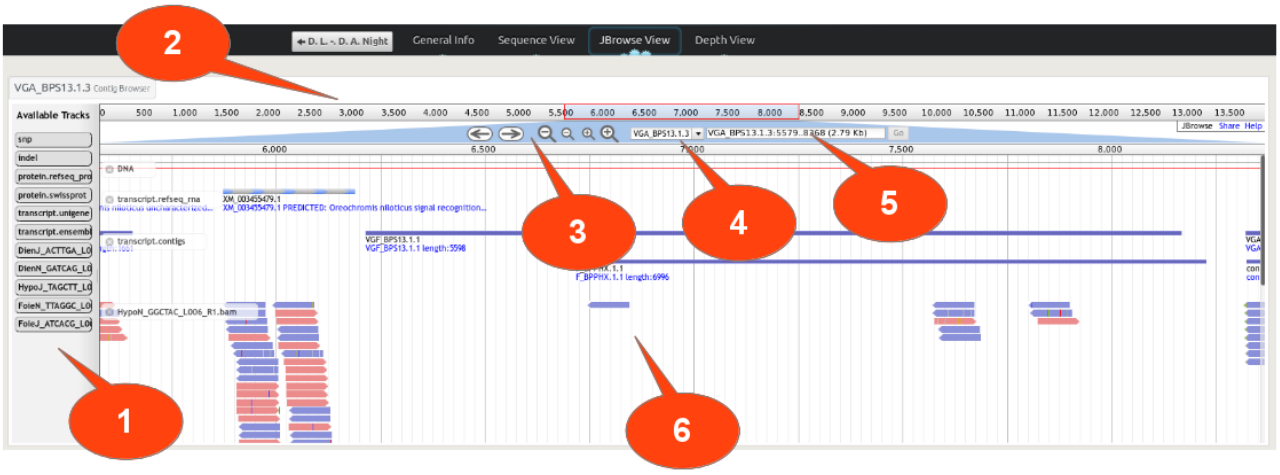
Contig jbrowse view

To give a graphical view of the annotations and other features on the contigs, jbrowse (a

genome browser) has been included in the environment. The jbrowse view uses the contig as reference and presents the features as different drawings on the reference.

The screen-shot hereunder presents the different elements of the jbrowse view :

1. the available tracks list presenting the features which can be displayed on the contig,
2. the reference ruler which enables to move on the reference by dragging the red rectangle,
3. the arrows to move to the left and right on the contig and the zoom in and out menu,
4. the browsed contig,
5. the location of the view on the contig,
6. the display panel.



To add a feature to the display panel simply drag and drop it from the available tracks list. To remove a feature click on the cross located at the left of the feature name.

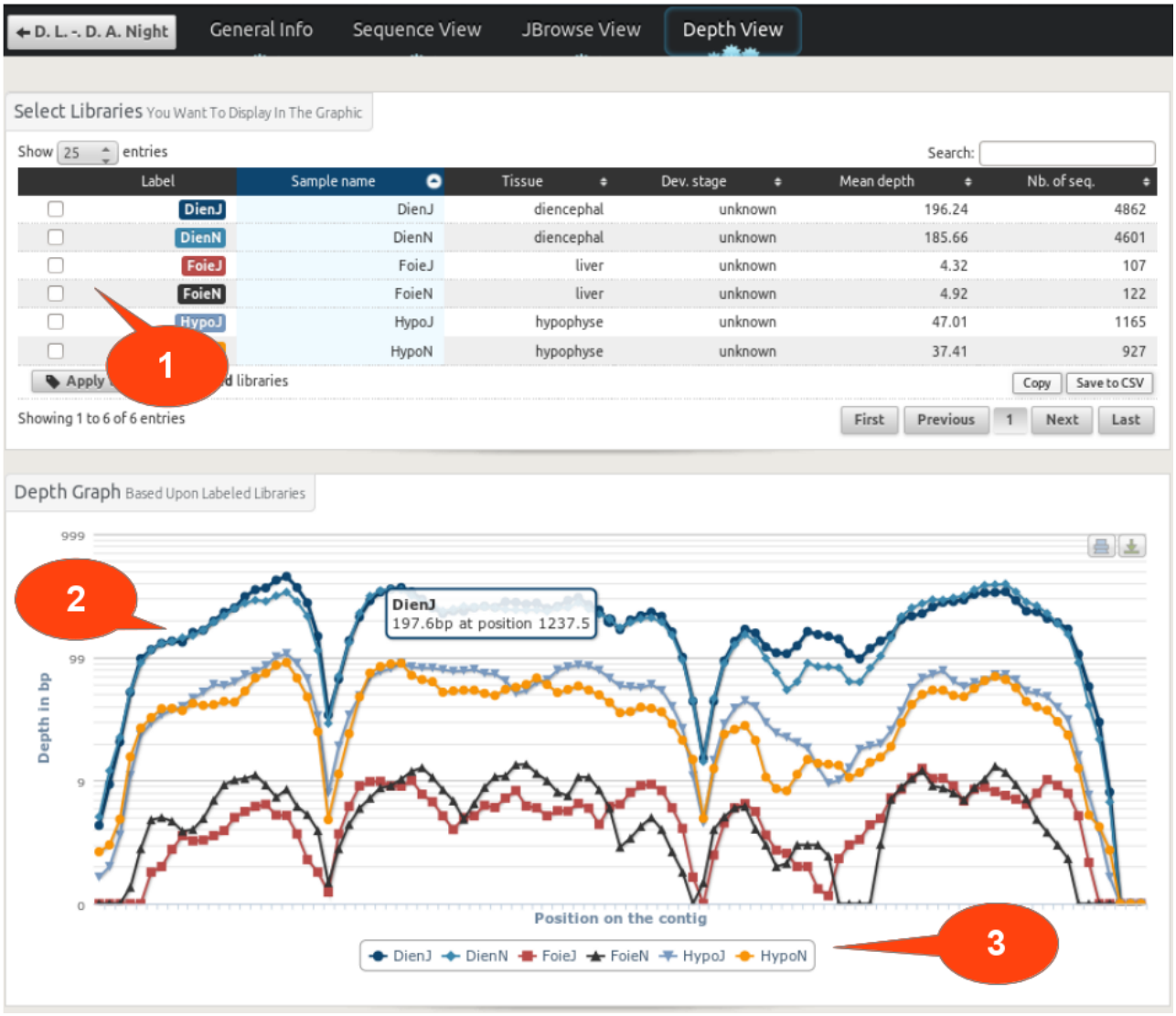
BEWARE : the bam file features can be very long to be displayed because of the read depth.

Contig depth view

The contig depth view enables to visualise the coverage of the reads of the different libraries on the contig. Each of the library has a colour in the table and on the graphic.

The screen-shot hereunder presents the different elements of the depth view :

1. the library table containing informations about the libraries such as average read depth and total number of sequences for the contig,
2. The graphical depth overview presents a different locations of the contig the depth of aligned sequences for each library,
3. the library can be removed or added to the graphical view by clicking on their name in the menu.



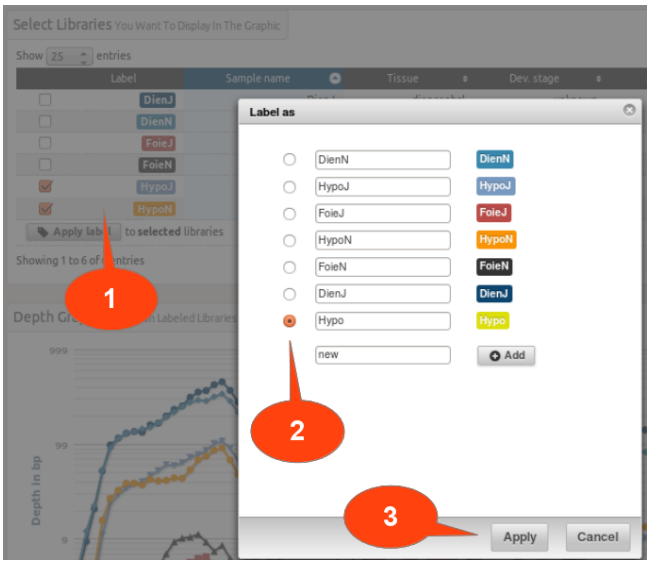
It is possible to modify the graphical layout by averaging different library depth.

(1) This is done by first ticking the check boxes in front of the libraries and the by clicking on the “apply label” button at the left bottom side of the table.

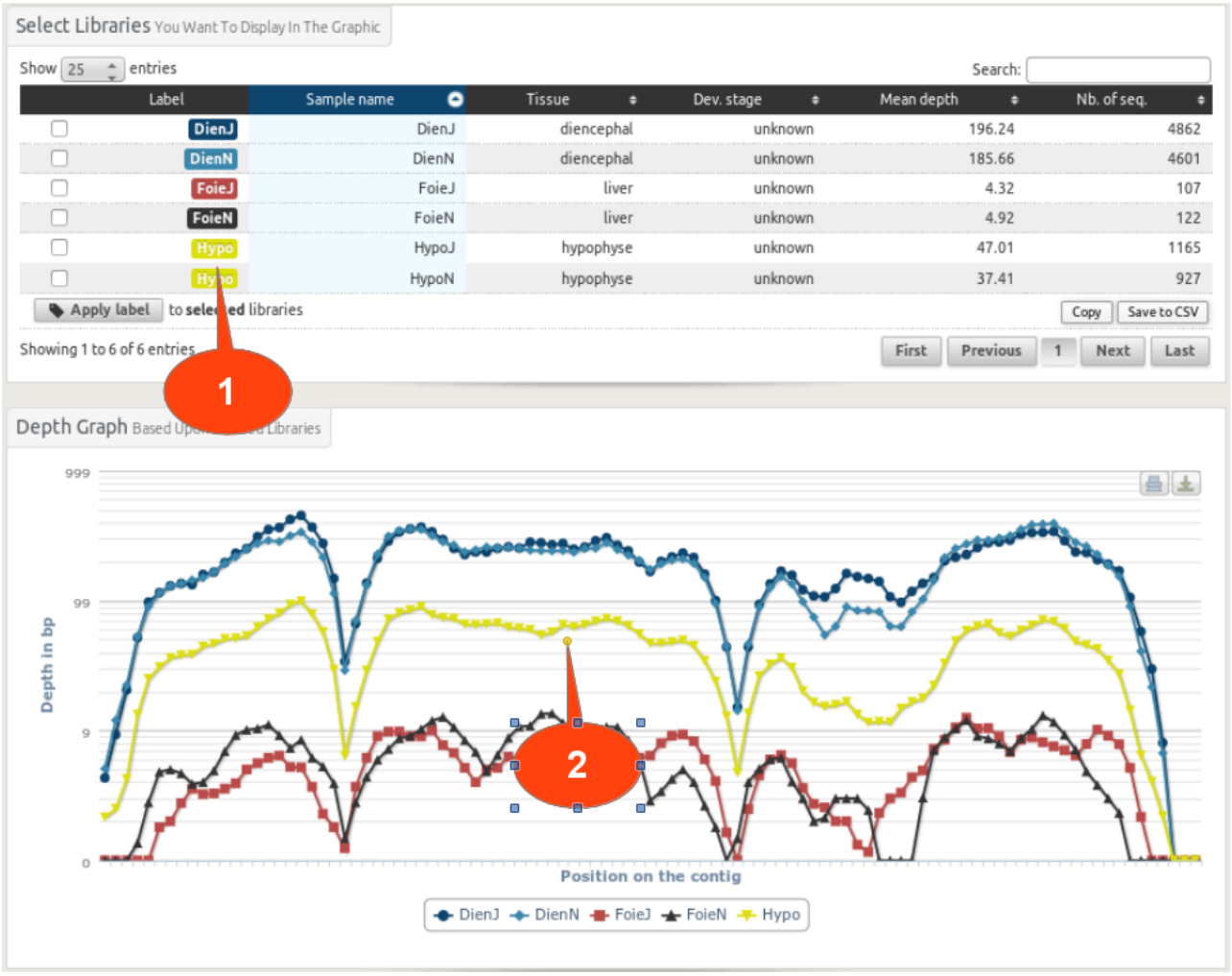
(2) The window present here will open and permit to select the name given to the previously select libraries or to create a new name using the add button.

(3) When the modification is applied the different libraries have the same name and the depth values in the graphic are the average depth values of these libraries.

This can typically be used when you want to merge replicates.



The table (1) and graphic (2) have been updated.



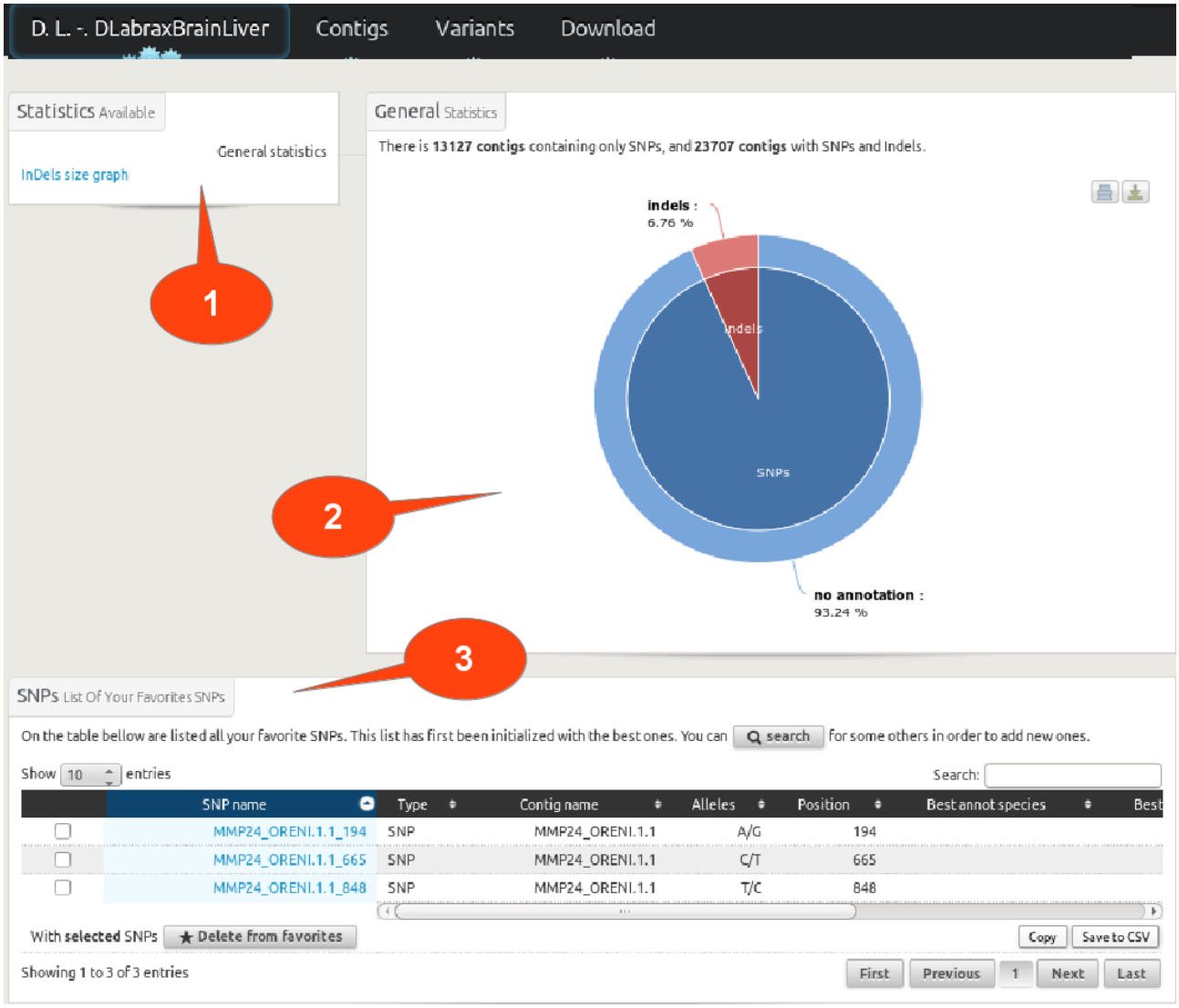
Variants page

The environment has also been design to be able to store and present variation related data. This is done in the Variants section presented in the global menu of the project (see screen-shot below).

Variants general information page

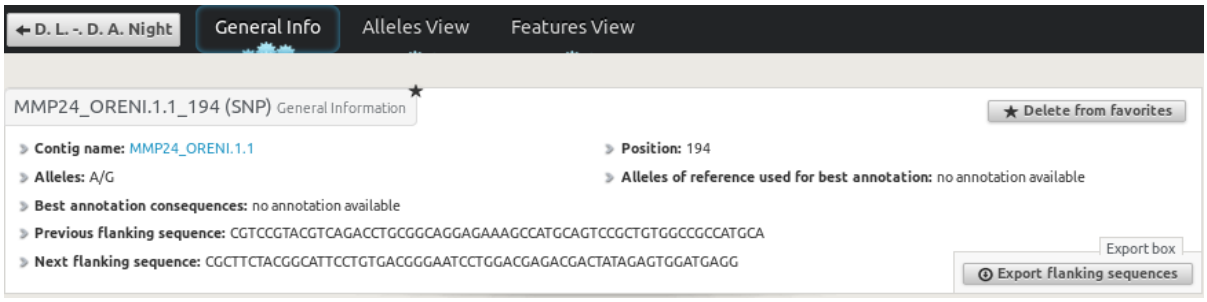
The elements numbered in the hereunder presented screen-shot correspond to :

1. menu of the table and graphics of the general statistic section,
2. general statistic graphical view
3. favourites SNP Indel table (the variation favourites are managed as the contig favourites).



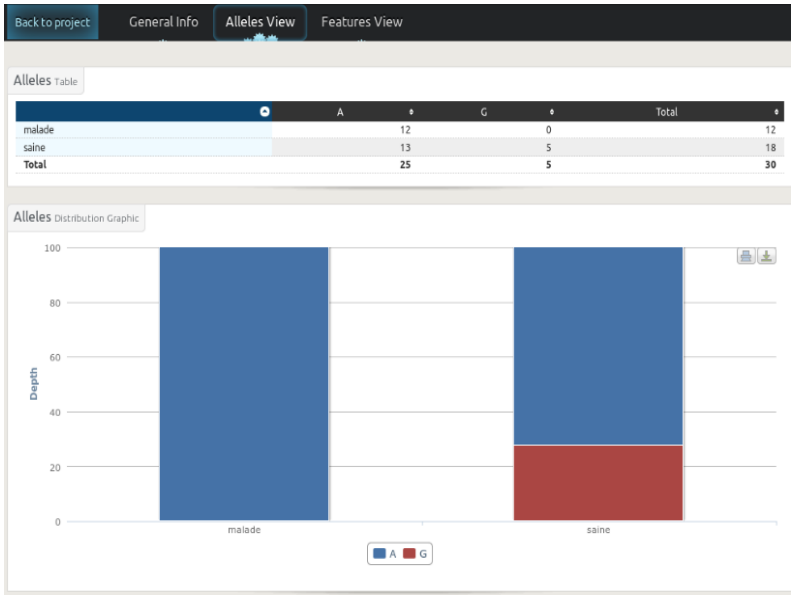
Variants general information view

The general information about a variation contains elements about de location, alleles, and flanking regions of the variation as shown in the next screen-shot.



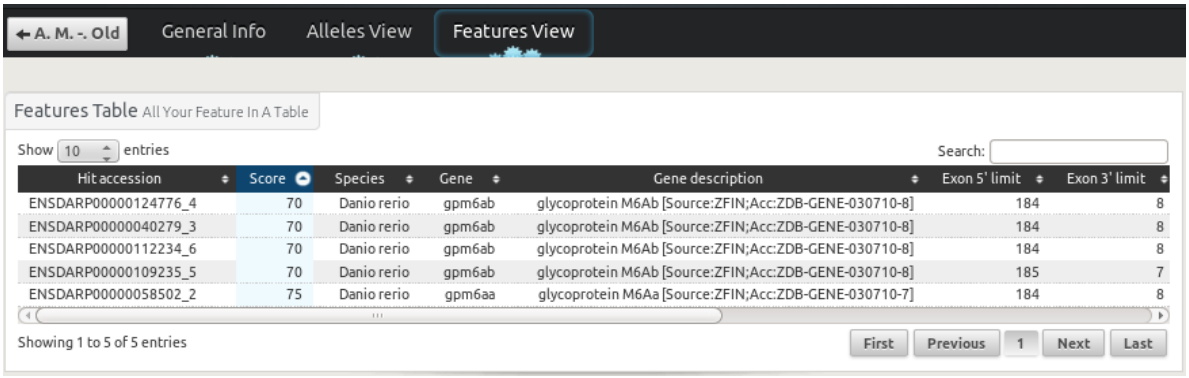
Variants allele view

For SNPs and Indels the allele view give allelic counts for the different libraries. The counts are shown on the top of the page in table and in a graphical manner at the bottom.



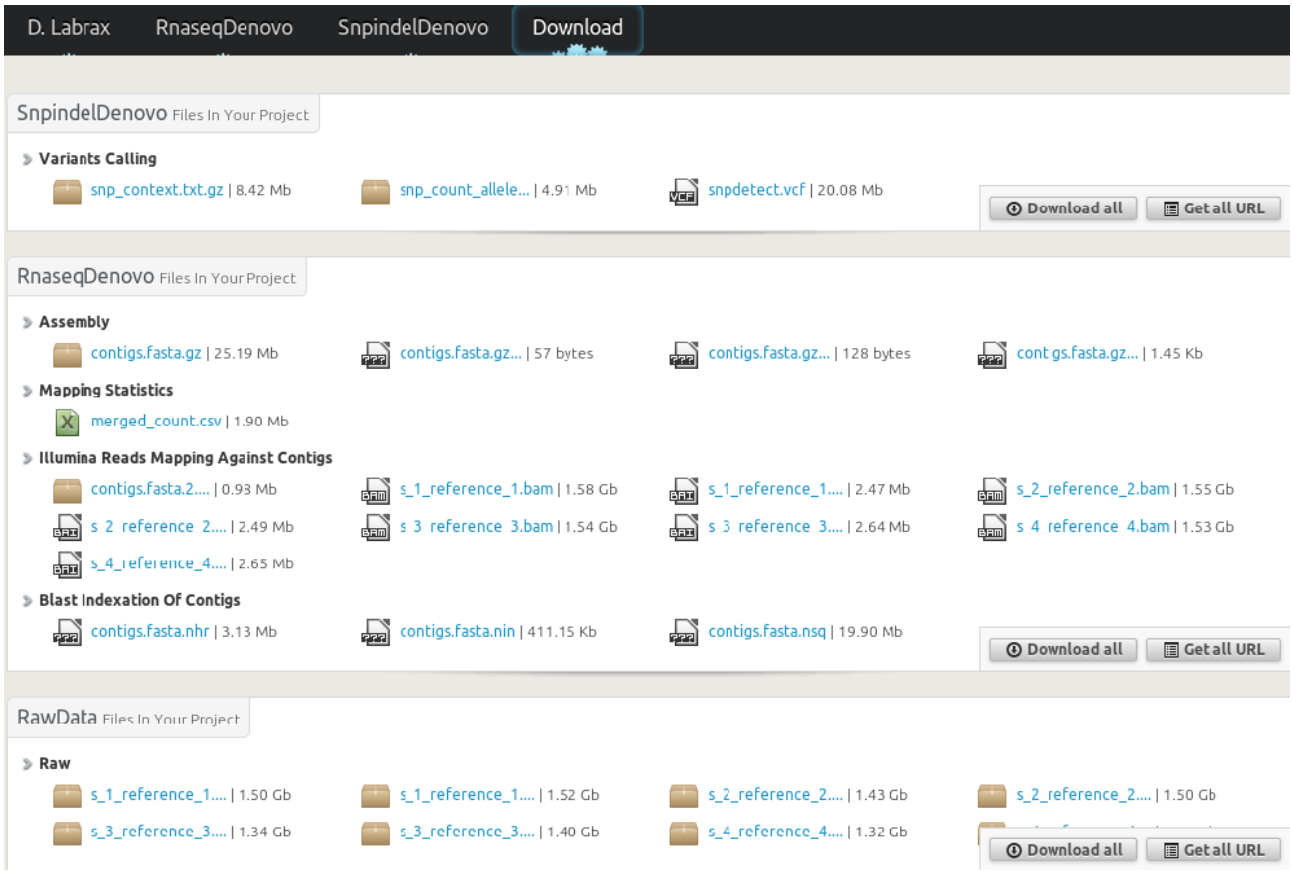
Variants feature view

The SNP feature view is meant to show annotation information about the SNP. It is often not functional for species not having closely related species with a genomic sequence.



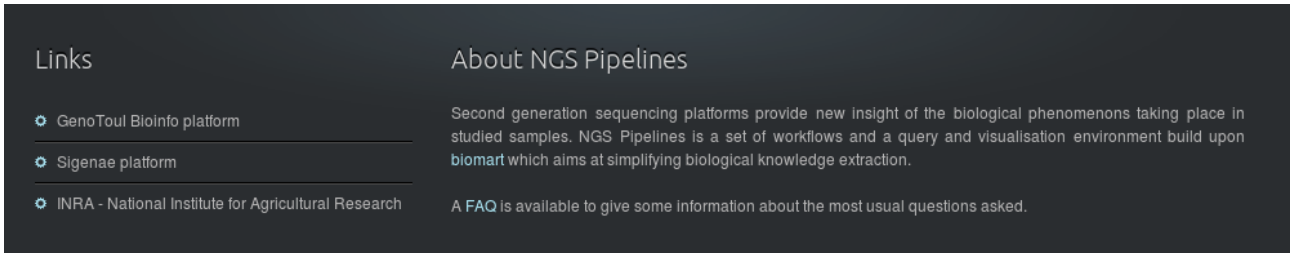
Download page

The download page can be access from the main menu of the environment. It is structured as presented in the next screen-shot.

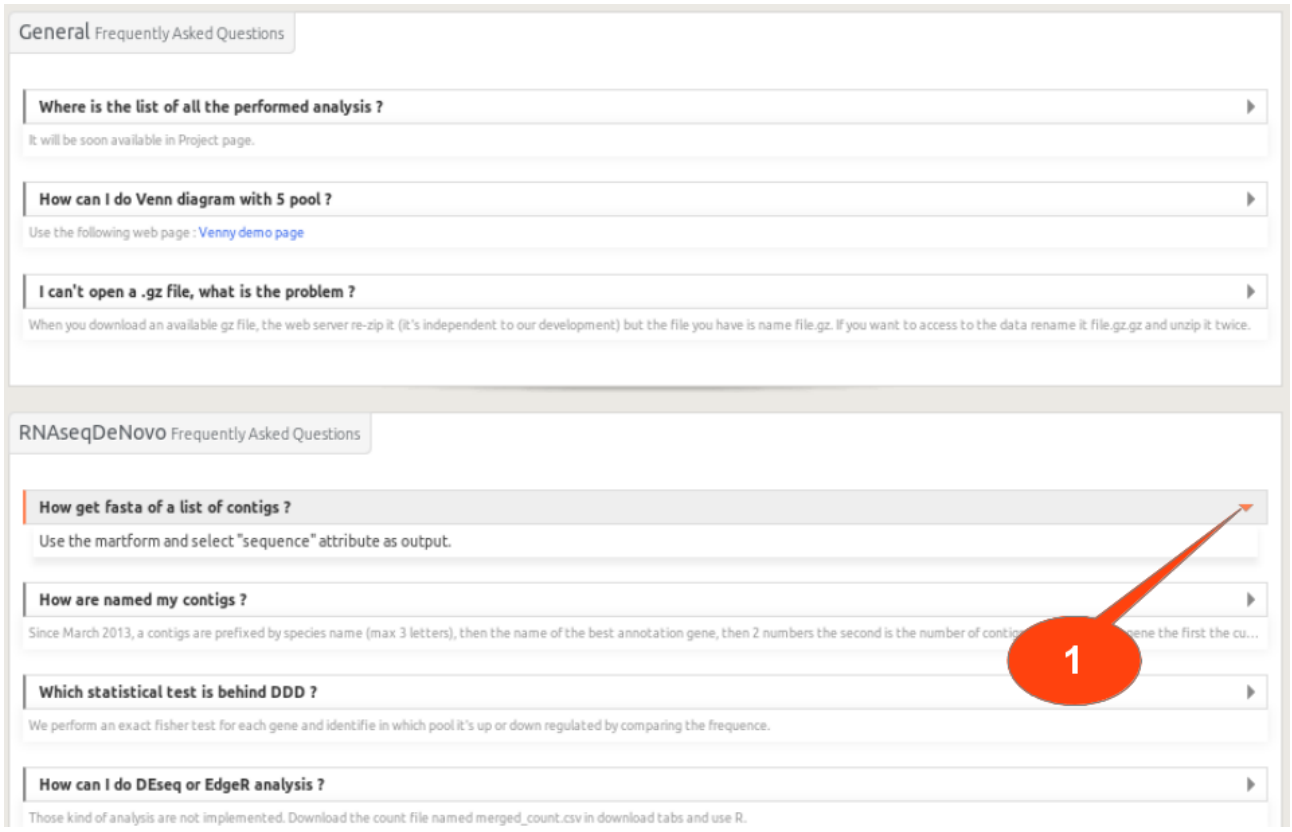


Frequently asked questions

A frequently asked question page is available from the footer of all pages.


Links
GenoToul Bioinfo platform
Sigenae platform
INRA - National Institute for Agricultural Research
About NGS Pipelines
Second generation sequencing platforms provide new insight of the biological phenomenons taking place in studied samples. NGS Pipelines is a set of workflows and a query and visualisation environment build upon biomart which aims at simplifying biological knowledge extraction.
A FAQ is available to give some information about the most usual questions asked.

The page gives an up-to-date list of questions and corresponding answers.


General Frequently Asked Questions
Where is the list of all the performed analysis ?
It will be soon available in Project page.
How can I do Venn diagram with 5 pool ?
Use the following web page : Venny demo page
I can't open a .gz file, what is the problem ?
When you download an available gz file, the web server re-zip it (it's independent to our development) but the file you have is name file.gz. If you want to access to the data rename it file.gz.gz and unzip it twice.
RNAseqDeNovo Frequently Asked Questions
How get fasta of a list of contigs ?
Use the martform and select "sequence" attribute as output.
How are named my contigs ?
Which statistical test is behind DDD ?
We perform an exact fisher test for each gene and identifie in which pool it's up or down regulated by comparing the frequence.
How can I do DEseq or EdgeR analysis ?
Those kind of analysis are not implemented. Download the count file named merged_count.csv in download tabs and use R.
1

Conclusion and future work

The RNAbrowse has been design to evolve with the users needs.
Some of them have already been defined including :

- micro-satellite annotation storage to complete the variation section
- Interproscan result storage

There are still some functionalities which are not working as they should :

- openID
- favourites for the logged users